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BIOTECHNOLOGY
SYSTEMS
BRANCH

#1.5

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/543,679
Art Unit / Team No. : O/PE
Date Processed by STIC: 4/25/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/543,679

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.

- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) **(2) INFORMATION FOR SEQ ID NO:X:**
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) **<210> sequence id number**
 <400> sequence id number
 000

- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)

- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

- 13 PatentIn ver. 2.0 "bug" **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/543,679

DATE: 04/25/2000
TIME: 12:25:58

INPUT SET: S35381.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

1
2
3 (1) General Information
4 (i) APPLICANT: East Carolina University
5 et al.
6 (ii) TITLE OF THE INVENTION: LOW ADENOSINE
7 OLIGONUCLEOTIDE AGENT,
8
9 TREATMENTS
10 (iii) NUMBER OF SEQUENCES: 3110
11 (iv) CORRESPONDENCE ADDRESS:
12 (A) ADDRESSEE: ARTER & HADDEN
13 (B) STREET: 725 South Figueroa St, #
14 3400
15 (C) CITY: Los Angeles
16 (D) STATE: CA
17 (E) COUNTRY: USA
18 (F) ZIP: 90071
19 (v) COMPUTER READABLE FORM:
20 (A) MEDIUM TYPE: Diskette
21 (B) COMPUTER: IBM Compatible
22 (C) OPERATING SYSTEM: DOS
23 (D) SOFTWARE: FastSEQ for Windows
24 Version 2.0
25 (vi) CURRENT APPLICATION DATA:
26 (A) APPLICATION NUMBER: PCT/US99/
27 (B) FILING DATE: 3-AUG-1999
28 (C) CLASSIFICATION: UNKNOWN
29 (vii) PRIOR APPLICATION DATA:
30 (A) APPLICATION NUMBER: 60/095,212
31 (B) FILING DATE: 03-AUG-1998
32 (viii) ATTORNEY/AGENT INFORMATION:
33 (A) NAME: Amzel, Viviana
34 (B) REGISTRATION NUMBER: 30,930
35 (C) REFERENCE/DOCKET NUMBER: EPI-109
36 (ix) TELECOMMUNICATION INFORMATION:
37 (A) TELEPHONE: 213-430-3520
38 (B) TELEFAX: 213-617-9255
39 (C) TELEX:
40

more up don't use TAB codes

FYI: all U.S. applications filed on or after July 1, 1998, and which do not claim a prior U.S. application or international application designating the United States, need to be in new Sequence Rules format

ERRORED SEQUENCES FOLLOW:

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/543,679DATE: 04/25/2000
TIME: 12:25:58

INPUT SET: S35381.raw

--> 41 (2) INFORMATION FOR SEQ ID NO:1:
42 (i) SEQUENCE CHARACTERISTICS:
43 (A) LENGTH: 21 base pairs
44 (B) TYPE: nucleic acid
45 (C) STRANDEDNESS: single
46 (D) TOPOLOGY: linear
47 (ii) MOLECULE TYPE: cDNA
48 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
49 GATGGAGGGC GGCATGGCGG G
50 21
51

*global
format error
→ 21*

--> 52 (2) INFORMATION FOR SEQ ID NO:2:
53 (i) SEQUENCE CHARACTERISTICS:
54 (A) LENGTH: 21 base pairs
55 (B) TYPE: nucleic acid
56 (C) STRANDEDNESS: single
57 (D) TOPOLOGY: linear
58 (ii) MOLECULE TYPE: cDNA
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
60 GTAGCAGGCG GGGATGGGGG C
61 21
62

same error

--> 63 (2) INFORMATION FOR SEQ ID NO:3:
64 (i) SEQUENCE CHARACTERISTICS:
65 (A) LENGTH: 18 base pairs
66 (B) TYPE: nucleic acid
67 (C) STRANDEDNESS: single
68 (D) TOPOLOGY: linear
69 (ii) MOLECULE TYPE: cDNA
70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
71 GTTGTTGGGC ATCTTGCC
72 18
73

same

--> 74 (2) INFORMATION FOR SEQ ID NO:4:
75 (i) SEQUENCE CHARACTERISTICS:
76 (A) LENGTH: 18 base pairs
77 (B) TYPE: nucleic acid
78 (C) STRANDEDNESS: single
79 (D) TOPOLOGY: linear
80 (ii) MOLECULE TYPE: cDNA
81 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
82 GTACTTGCGG ATCTAGGC
83 18
84

same

--> 85 (2) INFORMATION FOR SEQ ID NO:5:
86 (i) SEQUENCE CHARACTERISTICS:
87 (A) LENGTH: 18 base pairs
88 (B) TYPE: nucleic acid
89 (C) STRANDEDNESS: single

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/543,679DATE: 04/25/2000
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90 (D) TOPOLOGY: linear
91 (ii) MOLECULE TYPE: cDNA
92 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
93 GTGGGCCTAG CTCTCGCC
94 18
95

--> 96 (2) INFORMATION FOR SEQ ID NO:6:
97 (i) SEQUENCE CHARACTERISTICS:
98 (A) LENGTH: 18 base pairs
99 (B) TYPE: nucleic acid
100 (C) STRANDEDNESS: single
101 (D) TOPOLOGY: linear
102 (ii) MOLECULE TYPE: cDNA
103 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
104 GTCGGGGTAC CTGTCCGC
105 18
106

--> 107 (2) INFORMATION FOR SEQ ID NO:7:
108 (i) SEQUENCE CHARACTERISTICS:
109 (A) LENGTH: 21 base pairs
110 (B) TYPE: nucleic acid
111 (C) STRANDEDNESS: single
112 (D) TOPOLOGY: linear
113 (ii) MOLECULE TYPE: cDNA
114 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
115 CTCGTCGCCG TCGCCGGCGG G
116 21
117

--> 118 (2) INFORMATION FOR SEQ ID NO:8:
119 (i) SEQUENCE CHARACTERISTICS:
120 (A) LENGTH: 20 base pairs
121 (B) TYPE: nucleic acid
122 (C) STRANDEDNESS: single
123 (D) TOPOLOGY: linear
124 (ii) MOLECULE TYPE: cDNA
125 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
126 GGGTGGTGCT ATGTCCGGC
127 20
128

--> 129 (2) INFORMATION FOR SEQ ID NO:9:
130 (i) SEQUENCE CHARACTERISTICS:
131 (A) LENGTH: 15 base pairs
132 (B) TYPE: nucleic acid
133 (C) STRANDEDNESS: single
134 (D) TOPOLOGY: linear
135 (ii) MOLECULE TYPE: cDNA
136 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
137 GGCCAGGGC CAGCC
138 15

*same**✓*

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/543,679DATE: 04/25/2000
TIME: 12:25:59

INPUT SET: S35381.raw

139

140 (2) INFORMATION FOR SEQ ID NO:10:
141 (i) SEQUENCE CHARACTERISTICS:
--> 142 (A) LENGTH: 21 base pairs
143 (B) TYPE: nucleic acid
144 (C) STRANDEDNESS: single
145 (D) TOPOLOGY: linear
146 (ii) MOLECULE TYPE: cDNA
147 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
148 GGCCGGGCCA GCCGGGCCG G
149 21
150

151 (2) INFORMATION FOR SEQ ID NO:11:
152 (i) SEQUENCE CHARACTERISTICS:
--> 153 (A) LENGTH: 50 base pairs
154 (B) TYPE: nucleic acid
155 (C) STRANDEDNESS: single
156 (D) TOPOLOGY: linear
157 (ii) MOLECULE TYPE: cDNA
158 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
159 GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCTGGGC
160 50
161

162 (2) INFORMATION FOR SEQ ID NO:12:
163 (i) SEQUENCE CHARACTERISTICS:
--> 164 (A) LENGTH: 49 base pairs
165 (B) TYPE: nucleic acid
166 (C) STRANDEDNESS: single
167 (D) TOPOLOGY: linear
168 (ii) MOLECULE TYPE: cDNA
169 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
170 CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCTGGGC
171 49
172

173 (2) INFORMATION FOR SEQ ID NO:13:
174 (i) SEQUENCE CHARACTERISTICS:
--> 175 (A) LENGTH: 48 base pairs
176 (B) TYPE: nucleic acid
177 (C) STRANDEDNESS: single
178 (D) TOPOLOGY: linear
179 (ii) MOLECULE TYPE: cDNA
180 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
181 GGCCTGGAAG GCTGAGATGG AGGGCGGCAT GGCGGGCACA GGCTGGGC
182 48
183

184 (2) INFORMATION FOR SEQ ID NO:14:
185 (i) SEQUENCE CHARACTERISTICS:
--> 186 (A) LENGTH: 47 base pairs

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PATENT APPLICATION US/09/543,679DATE: 04/25/2000
TIME: 12:25:59

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187 (B) TYPE: nucleic acid
188 (C) STRANDEDNESS: single
189 (D) TOPOLOGY: linear
190 (ii) MOLECULE TYPE: cDNA
191 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
192 GCCTGGAAAAG CTGAGATGGA GGGCGGCATG GCGGGCACAG GCTGGGC
193 47
194

Same

--> 195 (2) INFORMATION FOR SEQ ID NO:15:
196 (i) SEQUENCE CHARACTERISTICS:
197 (A) LENGTH: 46 base pairs
198 (B) TYPE: nucleic acid
199 (C) STRANDEDNESS: single
200 (D) TOPOLOGY: linear
201 (ii) MOLECULE TYPE: cDNA
202 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
203 CCTGGAAAAGC TGAGATGGAG GCGGCATGG CGGGCACAGG CTGGGC
204 46
205

--> 206 (2) INFORMATION FOR SEQ ID NO:16:
207 (i) SEQUENCE CHARACTERISTICS:
208 (A) LENGTH: 45 base pairs
209 (B) TYPE: nucleic acid
210 (C) STRANDEDNESS: single
211 (D) TOPOLOGY: linear
212 (ii) MOLECULE TYPE: cDNA
213 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
214 CTGGAAAAGCT GAGATGGAGG GCGGCATGGC GGCACAGGC TGGGC
215 45
216

--> 217 (2) INFORMATION FOR SEQ ID NO:17:
218 (i) SEQUENCE CHARACTERISTICS:
219 (A) LENGTH: 44 base pairs
220 (B) TYPE: nucleic acid
221 (C) STRANDEDNESS: single
222 (D) TOPOLOGY: linear
223 (ii) MOLECULE TYPE: cDNA
224 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
225 TGGAAAGCTG AGATGGAGGG CCGCATGGCG GGCACAGGCT GGGC
226 44
227

--> 228 (2) INFORMATION FOR SEQ ID NO:18:
229 (i) SEQUENCE CHARACTERISTICS:
230 (A) LENGTH: 43 base pairs
231 (B) TYPE: nucleic acid
232 (C) STRANDEDNESS: single
233 (D) TOPOLOGY: linear
234 (ii) MOLECULE TYPE: cDNA
235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

*These errors
are global. See
item 1 on
Error Summary
sheet*

INPUT SET: S35381.raw

26157 8
26158

26159 (2) INFORMATION FOR SEQ ID NO:2420:
26160 (i) SEQUENCE CHARACTERISTICS:
--> 26161 (A) LENGTH: 981 base pairs
26162 (B) TYPE: nucleic acid
26163 (C) STRANDEDNESS: single
26164 (D) TOPOLOGY: linear
26165 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2420:
26166 1 ATGCCGCCCT CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT
26167 GCTCATCGGC
26168 61 CTGGTCTCTG TGCCCGGGAA CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA
26169 CCAGGCGCTG
26170 121 CGGGATGCCA CCTTCTGCTT CATCGTCTCG CTGGCGGTGG CTGATGTGGC
26171 CGTGGGTGGC
26172 181 CTGGTCATCC CCCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT
26173 CCACACCTGG
26174 241 CTCATGGTTG CCTGTCCGGT CCTCATCCTC ACCCAGAGCT CCATCCTGGC
26175 CCTGCTGGCA
26176 301 ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT
26177 GGTGGTGAAC
26178 361 CCCCCGAGGG CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT
26179 GGTGGGACTG
26180 421 ACCCCTATGT TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGGC
26181 AGCCAAGGGC
26182 481 AGCATGGGGG AGCCCGTGAT CAAGTGCGAG TTCGAGAAGG TCATCAGCAT
26183 GGAGTACATG
26184 541 GTCTACTTCA ACTTCTTTGT GTGGGTGCTG CCCCCGCTTC TCCTCATGGT
26185 CCTCATCTAC
26186 601 CTGGAGGTCT TCTACCTAAT CCGCAAGCAG CTCAACAAGA AGGTGTCGGC
26187 CTCTTCGGC
26188 661 GACCCGCAGA AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC
26189 CCTCATCTCT
26190 721 TTCTCTTTG CCCTCAGCTG GCTGCCTTTG CACATCCTCA ACTGCATCAC
26191 CCTCTCTGTC
26192 781 CCGTCTTGCC ACAAGCCCAG CATCCTTACC TACATTGCCA TCTTCCTCAC
26193 GCACGGCAAC
26194 841 TCGGCCATGA ACCCATTTGT CTATGCCTTC CGCATCCAGA AGTTCCGCGT
26195 CACCTTCCTT
26196 901 AAGATTTGGA ATGACCATTT CCGCTGCCAG CCTGCACCTC CCATTGACGA
26197 GGATCTCCCA
26198 961 GAAGAGAGGC CTGATGACTA G
26199

? what format
is
this?
60
120

Cumulative
base totals,
per sequence
Runs, need
to be at
right margin
of each line

26200 (2) INFORMATION FOR SEQ ID NO:2421:
26201 (i) SEQUENCE CHARACTERISTICS:
--> 26202 (A) LENGTH: 2900 base pairs
26203 (B) TYPE: nucleic acid
26204 (C) STRANDEDNESS: single
26205 (D) TOPOLOGY: linear
26206 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2421:
26207 1 ATGAGTGTCA GAAGTGTGAA GGGTGCCTGT TCTGAATCCC AGAGCCTCCT

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/543,679DATE: 04/25/2000
TIME: 12:29:08

INPUT SET: S35381.raw

26208 CTCCTCTGT
26209 61 GAGGCTGGCA GGTGAGGAAG GGTTTAACCT CACTGGAAGG AATCCCTGGA
26210 GCTAGCGGCT
26211 121 GCTGAAGGCG TCGAGGTGTG GGGGCACTTG GACAGAACAG TCAGGCAGCC
26212 GGGAGCTCTG
26213 181 CCAGCTTTGG TGACCTTGGG CCGGGCTGGG AGCGCTGCGG CGGGAGCCGG
26214 AGGACTATGA
26215 241 GCTGCCGCGC GTTGTCCAGA GCCCAGCCCA GCCCTACGCG CGCGGCCCGG
26216 AGCTCTGTTC
26217 301 CCTGGAACCT TGGGCACTGC CTCTGGGACC CCTGCCGGCC AGCAGGCAGG
26218 ATGGTGCTTG
26219 361 CCTCGTGCCC CTTGGTGCCC GTCTGCTGAT GTGCCCAGCC TGTGCCCCGG
26220 ATGCCGCCCT
26221 421 CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC
26222 CTGGTCTCTG
26223 481 TGCCCGGGA CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG
26224 CGGGATGCCA
26225 541 CCTTCTGCTT CATCGTGTCT CTGGCGGTGG CTGATGTGGC CGTGGGTGCC
26226 CTGGTCATCC
26227 601 CCCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT CCACACCTGC
26228 CTCATGGTTG
26229 661 CCTGTCCGGT CCTCATCCTC ACCCAGAGCT CCATCCTGGC CCTGCTGGCA
26230 ATTGCTGTGG
26231 721 ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGGTGACC
26232 CCCCCGAGGG
26233 781 CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT GGTGGGACTG
26234 ACCCCTATGT
26235 841 TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGGC AGCCAACGGC
26236 AGCATGGGGG
26237 901 AGCCCGTGAT CAAGTGCGAG TTCGAGAAGG TCATCAGCAT GGAGTACATG
26238 GTCTACTTCA
26239 961 ACTTCTTTGT GTGGGTGCTG CCCCCGCTTC TCCTCATGGT CCTCATCTAC
26240 CTGGAGGTCT
26241 1021 TCTACCTAAT CCGCAAGCAG CTCAACAAGA AGGTGTCGGC CTCCTCCGGC
26242 GACCCGCAGA
26243 1081 AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC CCTCATCCTC
26244 TTCCTCTTTG
26245 1141 CCCTCAGCTG GCTGCCTTTG CACATCCTCA ACTGCATCAC CCTCTTCTGC
26246 CCGTCCTGCC
26247 1201 ACAAGCCCAG CATCCTTACC TACATTGCCA TCTTCCTCAC GCACGGCAAC
26248 TCGGCCATGA
26249 1261 ACCCCATTGT CTATGCCTTC CGCATCCAGA AGTTCCGCGT CACCTTCCTT
26250 AAGATTTGGA
26251 1321 ATGACCATTT CCGCTGCCAG CCTGCACCTC CCATTGACGA GGATCTCCCA
26252 GAAGAGAGGC
26253 1381 CTGATGACTA GACCCCGCCT TCCGCTCCCA CCAGCCCACA TCCAGTGGGG
26254 TCTCAGTCCA
26255 1441 GTCCTCACAT GCCCGCTGTC CCAGGGGTCT CCCTGAGCCT GCCCCAGCTG
26256 GGCTGTTGGC
26257 1501 TGGGGGCATG GGGGAGGCTC TGAAGAGATA CCCACAGAGT GTGGTCCCTC
26258 CACTAGGAGT
26259 1561 TAACTACCCT ACACCTCTGG GCCCTGCAGG AGGCCTGGGA GGGCAAGGGT
26260 CCTACGGAGG

*Same
enum*

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/543,679DATE: 04/25/2000
TIME: 12:29:08

INPUT SET: S35381.raw

26261 1621 GACCAGGTGT CTAGAGGCAA CAGTGTCTG AGCCCCACC TGCCTGACCA
26262 TCCCATGAGC
26263 1681 AGTCCAGCGC TTCAGGGCTG GGCAGGTCCT GGGGAGGCTG AGACTGCAGA
26264 GGAGCCACCT
26265 1741 GGGCTGGGAG AAGGTGCTTG GGCTTCTGCG GTGAGGCAGG GGAGTCTGCT
26266 TGTCTTAGAT
26267 1801 GTTGGTGGTG CAGCCCCAGG ACCAAGCTTA AGGAGAGGAG AGCATCTGCT
26268 CTGAGACGGA
26269 1861 TGGAAGGAGA GAGGTTGAGG ATGCACTGGC CTGTTCTGTA GGAGAGACTG
26270 GCCAGAGGCA
26271 1921 GCTAAGGGGC AGGAATCAAAG GAGCCTCCGT TCCCACCTCT GAGGACTCTG
26272 GACCCCAGGC
26273 1981 CATACCAGGT GCTAGGGTGC CTGCTCTCCT TGCCCTGGGC CAGCCCAGGA
26274 TTGTACGTGG
26275 2041 GAGAGGCAGA AAGGGTAGGT TCAGTAATCA TTTCTGATGA TTTGCTGGAG
26276 TGCTGGCTCC
26277 2101 ACGCCCTGGG GAGTGAGCTT GGTGCGGTAG GTGCTGGCCT CAAACAGCCA
26278 CGAGGTGGTA
26279 2161 GCTCTGAGCC CTCCTTCTTG CCCTGAGCTT TCCGGGGAGG AGCCTGGAGT
26280 GTAATTACCT
26281 2221 GTCATCTGGG CCACCAGCTC CACTGGCCCC CGTTGCCGGG CCTGGACTGT
26282 CCTAGGTGAC
26283 2281 CCCATCTCTG CTGCTTCTGG GCCTGATGGA GAGGAGAACA CTAGACATGC
26284 CAACTCGGGA
26285 2341 GCATTCTGCC TGCCTGGGAA CGGGGTGGAC GAGGGAGTGT CTGTAAGGAC
26286 TCAGTGTGTA
26287 2401 CTGTAGGCGC CCCTGGGGTG GGTTTAGCAG GCTGCAGCAG GCAGAGGAGG
26288 AGTACCCCCC
26289 2461 TGAGAGCATG TGGGGGAAGG CCTTGCTGTC ATGTGAATCC CTCAATACCC
26290 CTAGTATCTG
26291 2521 GCTGGGTTTT CAGGGGCTTT GGAAGCTCTG TTGCAGGTGT CCGGGGGTCT
26292 AGGACTTTAG
26293 2581 GGATCTGGGA TCTGGGGAAG GACCAACCCA TGCCCTGCCA AGCCTGGAGC
26294 CCCTGTGTTG
26295 2641 GGGGGCAAGG TGGGGGAGCC TGGAGCCCCCT GTGTGGGAGG GCGAGGCGGG
26296 GGAGCCTGGA
26297 2701 GCCCCTGTGT GGGAGGGCGA GCGGGGGGAT CCTGGAGCCC CTGTGTCGGG
26298 GGGCGAGGGA
26299 2761 GGGGAGGTGG CCGTCGGTTG ACCTTCTGAA CATGAGTGTC AACTCCAGGA
26300 CTTGCTTCCA
26301 2821 AGCCCTTCCC TCTGTTGGAA ATTGGGTGTG CCCTGGCTCC CAAGGGAGGC
26302 CCATGTGACT
26303 2881 AATAAAAAAC TGTGAACCCT
26304

done

26305 (2) INFORMATION FOR SEQ ID NO:2422:
26306 (i) SEQUENCE CHARACTERISTICS:
--> 26307 (A) LENGTH: 1942 base pairs
26308 (B) TYPE: nucleic acid
26309 (C) STRANDEDNESS: single
26310 (D) TOPOLOGY: linear
26311 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2422:
26312 1 CGCATTTGTG TTTTAATAAA AGAATCTGGA AGATAAATAG TCTTGAAGAG

done

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/543,679DATE: 04/25/2000
TIME: 12:29:09

INPUT SET: S35381.raw

26313 AGACAAAGGA
26314 61 AGGAAAATTT AAATCCTTAG ATTCAAGCAG AAGAAATCCA TGTGGAAGGT
26315 TTGGGTGTGTT
26316 121 GTTGTGTGTTG TTTGGTGTGT TTTTGTGTTT TTTGTTTTTT TGTTTTTTTTT
26317 TGAGATGGAG
26318 181 TCTCGCTGTG TTACCGGGAG CGACAGAGCC GCACGGCCGA GTCGAGTCCC
26319 AGCCAGCTAC
26320 241 CATCCCTCTG GAGCTTACCG GCCGGCCTTG GCTTCCCCAG GAATCCCTGG
26321 AGCTAGCGGC
26322 301 TGCTGAAGGC GTCGAGGTGT GGGGGCACTT GGACAGAACA GTCAGGCAGC
26323 CGGGAGCTCT
26324 361 GCCAGCTTTG GTGACCTTGG GTGCTTGCCT CGTGCCCCCTT GGTGCCCCGTC
26325 TGCTGATGTG
26326 421 CCCAGCCTGT GCGCGCCATG CCGCCCTCCA TCTCAGCTTT CCAGGCCGCC
26327 TACATCGGCA
26328 481 TCGAGGTGCT CATCGCCCTG GTCTCTGTGC CCGGGAACGT GCTGGTGTATC
26329 TGGGCGGTGA
26330 541 AGGTGAACCA GCGCTGCGG GATGCCACCT TCTGCTTCAT CGTGTGCTG
26331 GCGGTGCGTG
26332 601 ATGTGGCCGT GGGTGCCCTG GTCATCCCCC TCGCCATCCT CATCAACATT
26333 GGGCCACAGA
26334 661 CCTACTTCCA CACCTGCCTC ATGGTTGCCT GTCCGGTCCT CATCCTCACC
26335 CAGAGCTCCA
26336 721 TCCTGGCCCT GCTGGCAATT GCTGTGGACC GCTACCTCCG GGTCAAGATC
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26338 781 ACAAGATGGT GGTGACCCCC CGGAGGGCGG CGGTGGCCAT AGCCGGCTGC
26339 TGGATCCTCT
26340 841 CCTTCGTGGT GGGACTGACC CCTATGTTTG GCTGGAACAA TCTGAGTGCG
26341 GTGGAGCGGG
26342 901 CCTGGGCAGC CAACGGCAGC ATGGGGGAGC CCGTGATCAA GTGCGAGTTC
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26344 961 TCAGCATGGA GTACATGGTC TACTTCAACT TCTTTGTGTG GGTGCTGCCC
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26346 1021 TCATGGTCCT CATCTACCTG GAGGTCTTCT ACCTAATCCG CAAGCAGCTC
26347 AACAAGAAGG
26348 1081 TGTCGGCCTC CTCCGGCGAC CCGCAGAAGT ACTATGGGAA GGAGCTGAAG
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26360 1441 CCCACATCCA GTGGGGTCTC AGTCCAGTCC TCACATGCCC GCTGTCCCAG
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26362 1501 GAGCCTGCCC CAGCTGGGCT GTTGGCTGGG GGCATGGGGG AGGCTCTGAA
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26364 1561 CAGAGTGTGG TCCCTCCACT AGGAGTTAAC TACCCTACAC CTCTGGGCCC
26365 TGCAGGAGGC

Done

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/543,679DATE: 04/25/2000
TIME: 12:29:09

INPUT SET: S35381.raw

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26372 1801 GGCAGGGGAG TCTGCTTGTC TTAGATGTTG GTGGTGCAGC CCCAGGACCA
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26374 1861 GAGGAGAGCA TCTGCTCTGA GACGGATGGA AGGAGAGAGG TTGAGGATGC
26375 ACTGGCCTGT
26376 1921 TCTGTAGGAG AGACTGGCCA GA
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*Please correct this type of error
in subsequent sequence?*

--> 26380 (2) INFORMATION FOR SEQ ID NO:2423:
26379 (i) SEQUENCE CHARACTERISTICS:
26381 (A) LENGTH: 5904 base pairs
26382 (B) TYPE: nucleic acid
26383 (C) STRANDEDNESS: single
26384 (D) TOPOLOGY: linear
26385 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2423:
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26409 GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG TGCCCGGGAA CGTGCTGGTG
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26415 TGCTGGATCC TCTCCTTCGT GGTGGGACTG ACCCCTATGT TTGGCTGGAA CAATCTGAGT
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*where
are
cumulative
base totals?*

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/543,679

DATE: 04/25/2000

TIME: 12:29:09

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PATENT APPLICATION US/09/543,679DATE: 04/25/2000
TIME: 12:29:10

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26471 CCTTACCTAC ATTGCCATCT TCCTCACGCA CGGCAACTCG GCCATGAACC CCATTGTCTA
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26486

same
Please correct this type of error
in subsequent sequences

--> 26487 (2) INFORMATION FOR SEQ ID NO:2424:
26488 (i) SEQUENCE CHARACTERISTICS:
26489 (A) LENGTH: 1687 base pairs
26490 (B) TYPE: nucleic acid
26491 (C) STRANDEDNESS: single
26492 (D) TOPOLOGY: linear
26493 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2424:
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26496 61 CGGCGGGTCT CACGCGGCTG CCCCTCGCCC GCGCGCCTT CGGTAGGGGG
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26520 781 ACTGAGCTGA TGGACCACTC GAGGACCACC CTCCAGCGGG AGATCCATGC
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26522 841 CTGGCCATGA TTGTGGGGAT TTTTGCCCTG TGCTGGTTAC CTGTGCATGC